IN THE CLAIMS

The following listing of claim will replace all prior versions, and listings, of claims in this application:

Claim 1 (Currently Amended): A system for searching for relationships between base sequences in genes, comprising:

a theoretical value calculating portion which calculates theoretical restriction fragment length values of known genes digested by restriction enzymes based on restriction enzyme data in which kinds of restriction enzymes, recognition sites recognized by the restriction enzymes, and restriction sites at which the restriction enzymes cut in the recognition sites are stored in a related manner, and base sequence data in which kinds of known genes and base sequences of the known genes are stored in a related manner, and outputs theoretical restriction fragment patterns in which the kinds of known genes, the kinds of restriction enzymes, and the theoretical restriction fragment length values are stored in a related manner, ~~and~~

a comparing portion which compares the theoretical restriction fragment patterns with measured restriction fragment patterns in which the kinds of restriction enzymes and measured restriction fragment length values obtained as a result of digesting a sample by the restriction enzymes followed by measurement are stored in a related manner, calculates the degree of similarity of the known genes to the sample, and outputs the degree of similarity as analysis result data,

an amplified sequence recognizing portion which reads pre-amplification base sequence data, and which produces post-amplification base sequence data based on primer data including recognition site data of primers used for the amplification, wherein said theoretical value calculating portion calculates the theoretical restriction fragment length values based on the post-amplification base sequence data, and

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a displaying portion that diagrammatically displays samples having a high degree of

similarity therebetween or displays a known gene and a sample having a high degree of

similarity therebetween in a related manner based on the analysis result data.

Claim 2 (Cancelled).

Claim 3 (Currently Amended): A The system for searching for relationships between

base sequences as claimed in claim 1 2, wherein said displaying portion displays samples

having a high degree of similarity therebetween or displays a known gene and a sample

having a high degree of similarity therebetween in a related manner by a dendrogram.

Claim 4 (Currently Amended): A The system for searching for relationships between

base sequences as claimed in claim 1, wherein said comparing portion calculates the degree

of similarity based on the theoretical restriction fragment patterns and the measured

restriction fragment patterns by using an unweighted-pair-group method with arithmetic

mean.

Claim 5 (Cancelled).

Claim 6 (Currently Amended): A method of searching for relationships between base

sequence in genes, comprising:

a theoretical value calculating step for calculating theoretical restriction fragment

length values of known genes digested by restriction enzymes based on restriction enzyme

data in which kinds of restriction enzymes, recognition sites recognized by the restriction

enzymes, and restriction sites at which the restriction enzymes cut in the recognition sites are

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stored in a related manner, and base sequence data in which kinds of known genes and base sequences of the known genes are stored in a related manner, and outputting theoretical restriction fragment patterns in which the kinds of known genes, the kinds of restriction enzymes, and the theoretical restriction fragment length values are stored in a related manner, ~~and~~

a comparing step for comparing the theoretical restriction fragment patterns with measured restriction fragment patterns in which the kinds of restriction enzymes and measured restriction fragment length values obtained as a result of digesting a sample by the restriction enzymes followed by measurement are stored in a related manner, calculating the degree of similarity of the known genes to the sample, and outputting it as analysis result data,

an amplified sequence recognizing step for reading pre-amplification base sequence data, and producing post-amplification base sequence data based on primer data including recognition site data of the primers, wherein said theoretical value calculating step calculates the theoretical restriction fragment length values based on the post-amplification base sequence data, and

a displaying step for diagrammatically displaying samples having a high degree of similarity therebetween or a known gene and a sample having a high degree of similarity therebetween in a related manner based on the analysis result data.

Claim 7 (Cancelled).

Claim 8 (Currently Amended): ~~A~~ The method for searching for relationships between base sequences as claimed in claim 6 ~~7~~, wherein said displaying step displays samples having

a high degree of similarity therebetween or displays a known gene and a sample having a

high degree of similarity therebetween in a related manner by a dendrogram.

Claim 9 (Currently Amended): A The method for searching for relationships between

base sequences as claimed in claim 6, wherein said comparing step calculates the degree of

similarity based on the theoretical restriction fragment patterns and the measured restriction

fragment patterns by using an unweighted-pair-group method with arithmetic mean.

Claim 10 (Cancelled).

Claim 11 (Currently Amended): A recording medium readable on a computer having

recorded therein a computer program for implementing:

a theoretical value calculating step for calculating theoretical restriction fragment

length values of known genes digested by restriction enzymes based on restriction enzyme

data in which kinds of restriction enzymes, recognition sites recognized by the restriction

enzymes, and restriction sites at which the restriction enzymes cut in the recognition sites are

stored in a related manner, and base sequence data in which kinds of known genes and base

sequences of the known genes are stored in a related manner, and outputting theoretical

restriction fragment patterns in which the kinds of known genes, the kinds of restriction

enzymes, and theoretical restriction fragment length values are stored in a related manner,

and

a comparing step for comparing the theoretical restriction fragment patterns with

measured restriction fragment patterns in which the kinds of restriction enzymes and

measured restriction fragment length values obtained as a result of digesting a sample by the

restriction enzymes followed by measurement are stored in a related manner, calculating the

degree of similarity of the known genes to the sample, and outputting it as analysis result data,

an amplified sequence recognizing step for reading pre-amplification base sequence data, and producing post-amplification base sequence data by the primer based on primer data including a recognition site data of primers used for the amplification, wherein said theoretical value calculating step calculates the theoretical restriction fragment length values based on the post-amplification base sequence data, and

a displaying step for diagrammatically displaying samples having a high degree of similarity therebetween or diagrammatically displaying a known gene and a sample having a high degree of similarity therebetween in a related manner based on the analysis result data.

Claim 12 (Cancelled).

Claim 13 (Currently Amended): A The recording medium readable on a computer as claimed in claim 12 11, wherein said displaying step displays samples having a high degree of similarity therebetween or display a known gene and a sample having a high degree of similarity therebetween in a related manner by a dendrogram.

Claim 14 (Currently Amended): A The recording medium readable on a computer as claimed in claim 11, wherein said comparing step calculates the degree of similarity based on the theoretical restriction fragment patterns and the measured restriction fragment patterns by using an unweighted-pair-group method with arithmetic mean.

Claim 15 (Cancelled).